



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09 856 723
Source: OIE
Date Processed by STIC: 10/03/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER
VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND
TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: 09/856723
ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO		
1 <input type="checkbox"/> Wrapped Nucleics Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."	
2 <input type="checkbox"/> Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.	
3 <input type="checkbox"/> Misaligned Amino Numbering	The numbering under each 5 th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.	
4 <input type="checkbox"/> Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.	
5 <input type="checkbox"/> Variable Length	Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.	
6 <input type="checkbox"/> PatentIn 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s). Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.	
7 <input type="checkbox"/> Skipped Sequences (OLD RULES)	Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.	
8 <input type="checkbox"/> Skipped Sequences (NEW RULES)	Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence: <210> sequence id number <400> sequence id number 000	
9 <input checked="" type="checkbox"/> Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.	
10 <input type="checkbox"/> Invalid <213> Response	Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or Artificial Sequence	
11 <input type="checkbox"/> Use of <220>	Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)	
12 <input type="checkbox"/> PatentIn 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.	
13 <input type="checkbox"/> Misuse of n	n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.	

OIKE

RAW SEQUENCE LISTING

DATE: 10/03/2001

PATENT APPLICATION: US/09/856,723

TIME: 15:30:54

Input Set : A:\sequence listing 856723.7sept01.txt

Output Set: N:\CRF3\10032001\I856723.raw

3 <110> APPLICANT: Kramer, Michael
 5 <120> TITLE OF INVENTION: Regulatory Protein pKe#83 from Human
 6 Keratinocytes
 8 <130> FILE REFERENCE: km-3/PCT
 C--> 10 <140> CURRENT APPLICATION NUMBER: US/09/856,723
 C--> 11 <141> CURRENT FILING DATE: 2001-09-17
 13 <150> PRIOR APPLICATION NUMBER: DE19854672.6
 14 <151> PRIOR FILING DATE: 1998-11-26
 16 <150> PRIOR APPLICATION NUMBER: DE19856301.9
 17 <151> PRIOR FILING DATE: 1998-12-07
 19 <160> NUMBER OF SEQ ID NOS: 10
 21 <170> SOFTWARE: PatentIn Ver. 2.1

Does Not Comply
 Corrected Diskette Needed

Error: unknowns in line 599
 must enumerate unknowns

ERRORED SEQUENCES

"n" in a sequence must be described
 in fields 221, 222, and 223

512 <210> SEQ ID NO: 7
 513 <211> LENGTH: 4914
 514 <212> TYPE: DNA
 515 <213> ORGANISM: Homo sapiens
 517 <400> SEQUENCE: 7
 518 ggcgggggag cctccagaa taaccatcat atagccctg aggtggcatg gtgatgtctc 60
 519 catgaggga ccccttccca cttcatactg tcacgtatat catagtgttc ttgactgggc 120
 520 cattcatcta agatgggatt taccctgtga aacagggaga agacttatgg accccaagca 180
 521 tcatttcaag ttgaagttga gtttttaaaa gccatccatg caaagttcct ttgctttgga 240
 522 cctctgcat tattaaagct gctgtattgc taaccagaa ctgctccagt gtcttgactg 300
 523 atcatcatgg cttcagtttg gaagagactg cagcgtgtgg gaaaacatgc atccaagttc 360
 524 cagtttgttg cctcctacca ggagctcatg gttgagtgtg cgaagaaatg gtaaccagat 420
 525 aaactgggtg tagtttggac cagaagaagc cgaaggaagt cttctaaggc acatagctgg 480
 526 caacctggaa taaaaaatcc ctatcgtggg gttgttgtgt ggctgttcc tgaaaacatt 540
 527 gaaatcactg taacactttt taaggatcct catgcggaag aatttgaaga caaagagtgg 600
 528 acatttgtca tagaaaatga atcccttctt ggtcgaagga aagctcttgc tactagcagc 660
 529 atcaatatga aacagtatgc aagccctatg ccaactcaga ctgatgtcaa gttaaaattc 720
 530 aagccattat ctaaaaaagt tgtatctgcc gctcttcagt ttccattatc ttgcattttt 780
 531 ctgaggggaag gaaaagccac agatgaagac atgcaaagtt tggctagtgt ggtgagtatg 840
 532 aagcaggctg acattggcaa ttagatgac ttcgaagaag ataatagaaga tgatgatgag 900
 533 aacagagtga accaagaaga aaaggcagct aaaattacag agcttatcaa caaactaac 960
 534 tttttggatg aagcagaaaa ggacttggcc accgtgaatt caaatccatt tgatgatcct 1020
 535 gatgctgcag aattaaatcc atttggagat cctgactcag aagaacctat cactgaaaca 1080
 536 gcttcacctg gaaaaacaga agactctttt tataataaca gctataatcc ctttaaagag 1140
 537 gtgcagactc cacagtattt gaaccatttc gatgagccag aagcatttgt gaccataaag 1200
 538 gattctcttc ccagctctac aaaaagaaaa aatataagac ctgtggatat gagcaagtac 1260
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 542 ttaaatgaaa acacagtttc tgcaggaaaa gatctctcta cttctcttaa gccaaagcct 1500
 543 ataccaagtc ctgttttggg gcgaaagcca aatgctagtc agtctttgct tgtatggtgt 1560

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544 aaagaagtta caaagaacta ccgaggagta aaaatcacca attttactac atcgtggaga 1620
545 aatgggttat ctttttgtgc aatattacac cacttttagac cagatttaat tgactacaag 1680
546 tctctgaatc ctcaagatat taaagagaac aacaaaaagg catacgatgg atttgccagc 1740
547 ataggaatth cccgattatt ggaaccttct gatatggtat tattagcaat tcctgataaa 1800
548 ctgactgtta tgacttatct ctatcaaata agggcacatt tcagtggcca agaactaaat 1860
549 gtcgttcaga tagaggaaaa cagcagtaaa agcacatata aagttggaaa ctatgaaaca 1920
550 gatacaaaaca gttctgttga tcaagaaaaa ttctatgcag agcttagtga tctgaagcgg 1980
551 gagcctgaac tacaacagcc tatcagcggg gcagtagact tcttatcaca ggatgactct 2040
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553 caccttagtc caagcacagc ctcccttacc tgcgcagga ctaaaagtga cacagaacct 2160
554 cagaagtctc agcagagctc tggaggact tcaggatctg atgacctgg aatatgttcc 2220
555 aatacagatt caaccaagc acaggttttg ttaggcaaaa agagactatt gaaagctgag 2280
556 actttagaat tgagtgaact atatgttagt gataagaaga aggatatgtc tccacctttt 2340
557 atttgtgagg agacagatga acaaaagctt caaactctag acatcggtag taacttggag 2400
558 aaagaaaaat tagagaattc cagatcctta gaatgcagat cagatccaga atctcctatc 2460
559 aaaaaaacia gtttatctcc tacttctaaa cttggatact catatagtag agatctagac 2520
560 cttgctaaga aaaaacatgc ttccctgagg cagacggagt ctgatccaga tgctgataga 2580
561 accactttta atcatgcaga tcattcatca aaaatagtc agcatcgatt gttatctaga 2640
562 caagaagaac ttaaggaaag agcaagagtt ctgcttgagc aagcaagaag agatgcagcc 2700
563 ttaaaggcgg ggaataagca caataccaac acagccacct cattctgcaa caggcagcta 2760
564 agtgatcagc aagatgaaga gcgacgtcgg cagctgagag agagagctcg tcagctaata 2820
565 gcagaagctc gatctggagt gaagatgtca gaacttccca gctatggtga aatggctgca 2880
566 gaaaagttga aagaaaggtc aaaggcatct ggagatgaaa atgataatat tgagatagat 2940
567 actaacgagg agatccctga aggctttgtt gtaggaggtg gagatgaact tactaactta 3000
568 gaaaatgacc ttgatactcc cgaacaaaac agtaagttgg tggacttgaa gctgaagaag 3060
569 ctctagaag ttcagccaca ggtggcaaat tcacctcca gtgctgcca gaaagctgta 3120
570 actgagagct cagagcagga catgaaaagt ggcacagaag atctccggac tgaacgatta 3180
571 caaaaaacia cagaacgttt tagaaatcct gttgtgttca gcaaagattc tacagtcaga 3240
572 aaaactcaac ttcagtcttt cagccaatat attgagaata gaccagagat gaaaaggcag 3300
573 agatcaatac aggaagatac aaagaaagga aatgaggaga aggcagcgat aactgaaact 3360
574 cagaggaagc catcagaaga tgaagtgtt aataaaggtt tcaaagacac cagtcagtat 3420
575 gtagtaggag aattggcagc actagagaat gagcaaaagc aaattgacac ccgtgccgcg 3480
576 ctggtggaga agcgccttcg ctatctcatg gacacaggaa ggaacacaga agaagaagaa 3540
577 gctatgatgc aggaatggtt tatgttagtt aataagaaaa atgccttaat aaggagaatg 3600
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584 cagactcatt gttgatthaa aactthtaac attttgtttg gctggattgt actactttac 4020
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592 gtttttctgc agtggttgag tttcactgta aggataatgg agttcctctc ctctgctttc 4500

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593 ctacagaggat ggtccttttaa catagccaga aacaagccct gtggtttgaa ggtgagctgt 4560
594 gaggatggga ctaattgata tgcaccagtt tacaaagaca gtcttatcat ccgagaatac 4620
595 accatctttt tctctggata attatttctt acatcatgct tgattctac attttgttgg 4680
596 gtttcaacat tggctcacga atgctgttaa tatttattct gtattgataa aaagtctgtc 4740
597 ttgccactac aagtaaatec cccatttaat attttcttct ttagcatagc actgtcattt 4800
598 tttgtgaaaa tggttatggt tatttattac aatactgagt catatatataa ttttcaataa 4860
E--> 599 aagcagaaac tttcttacct taaaaaaaaa aaaaaaaaaa aaaaaaaaaa aad 4914

↓
invalid

VERIFICATION SUMMARY

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TIME: 15:30:55

Input Set : A:\sequence listing 856723.7sept01.txt

Output Set: N:\CRF3\10032001\I856723.raw

L:10 M:270 C: Current Application Number differs, Replaced Current Application Number
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:599 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:7
L:599 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1